

FIG. 1A

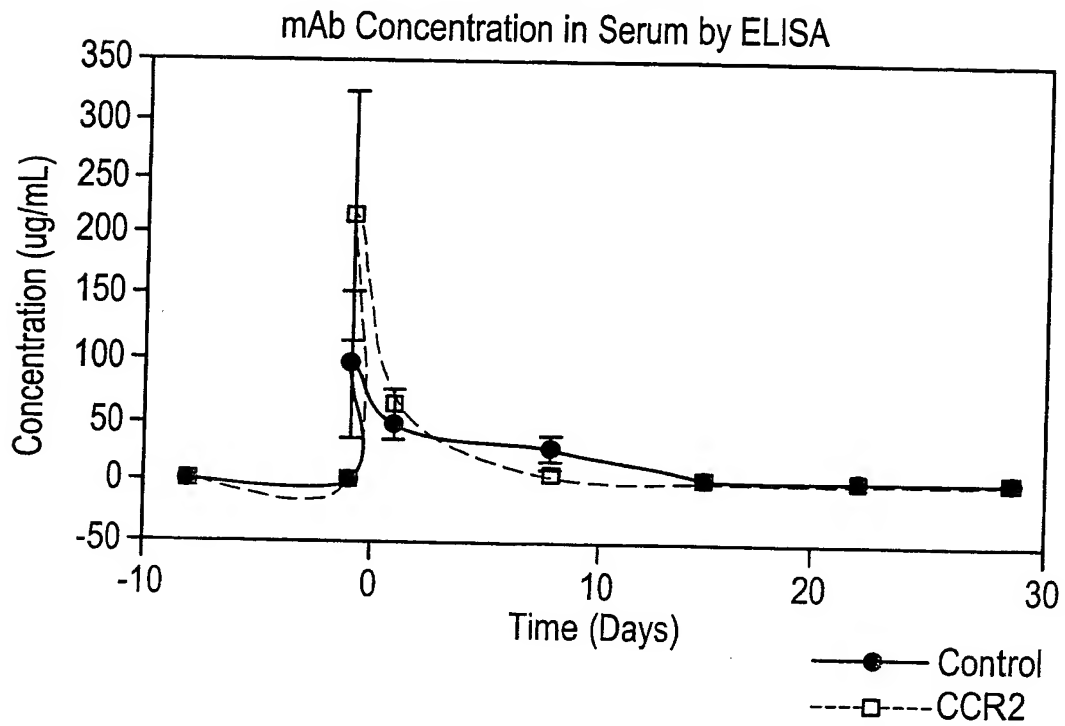


FIG. 1B

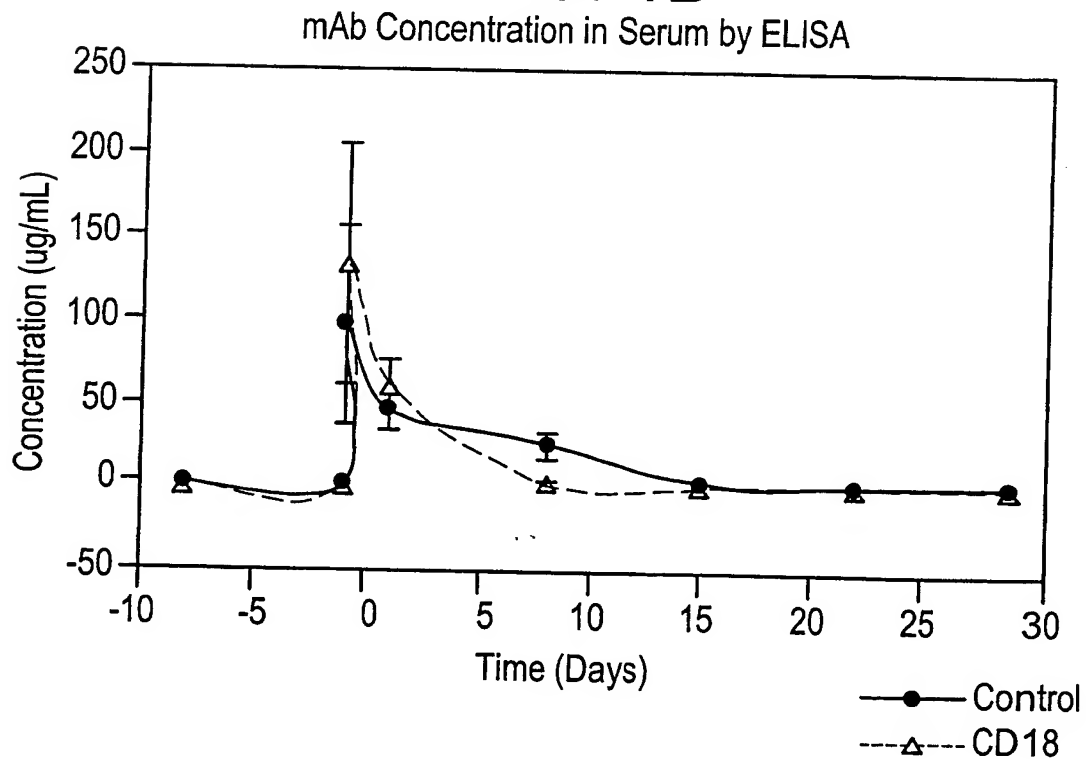


FIG. 2A

Monocyte Free Target Sites

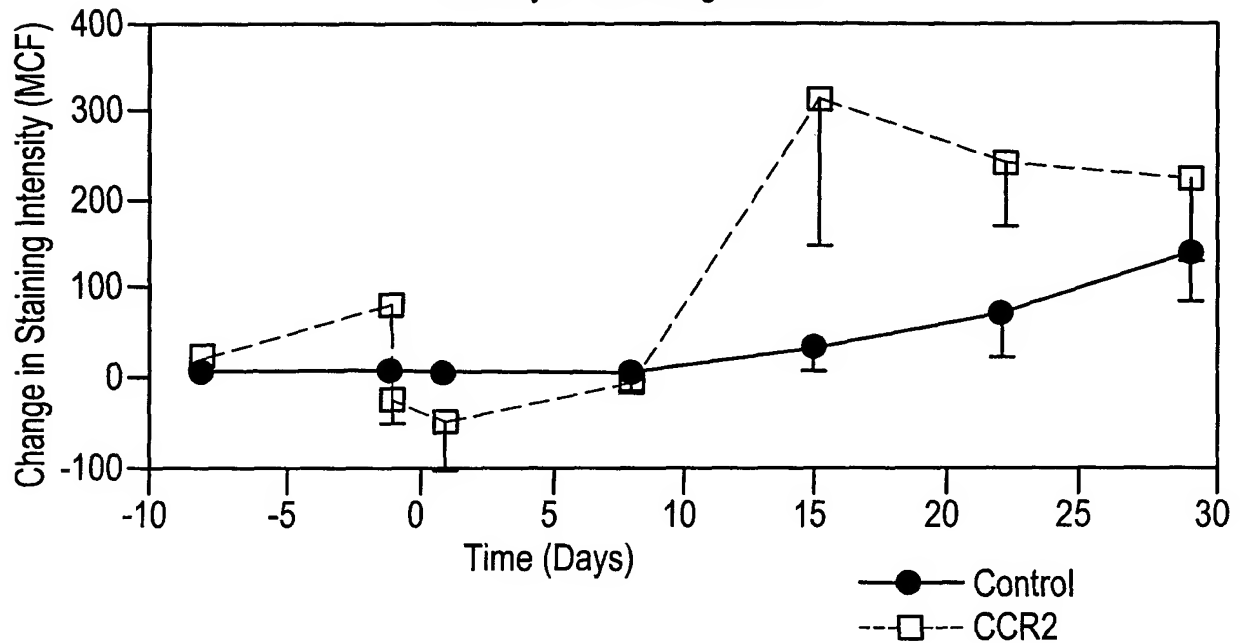


FIG. 2B

Neutrophil Free Target Sites

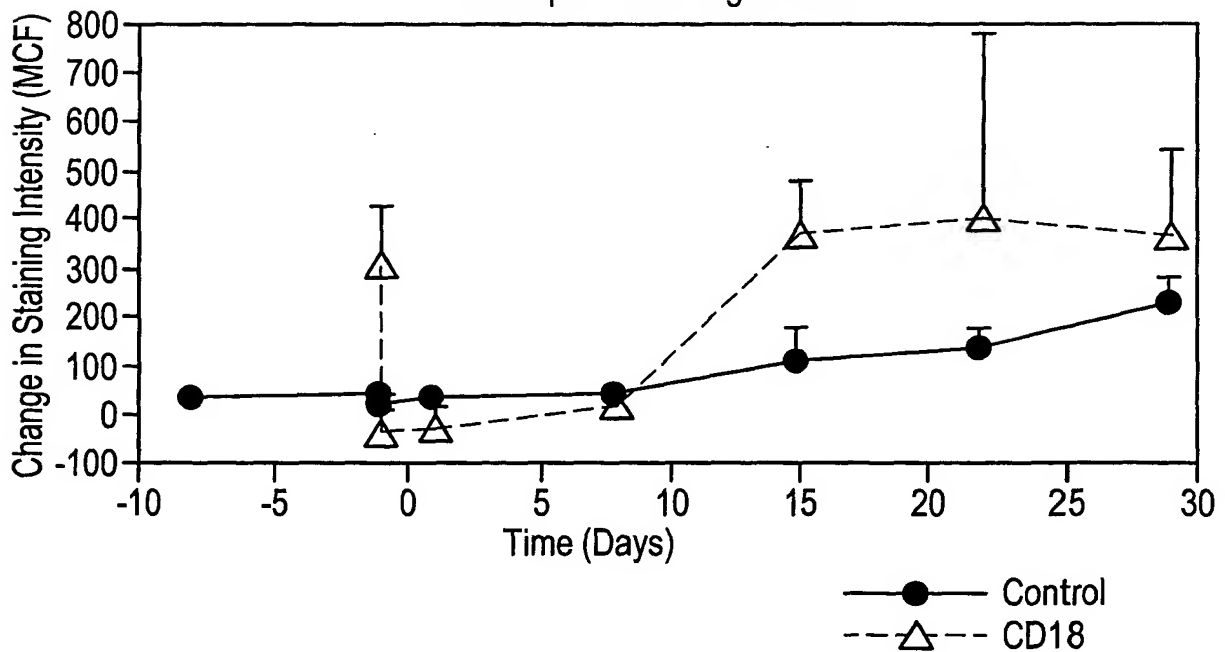


FIG. 2C

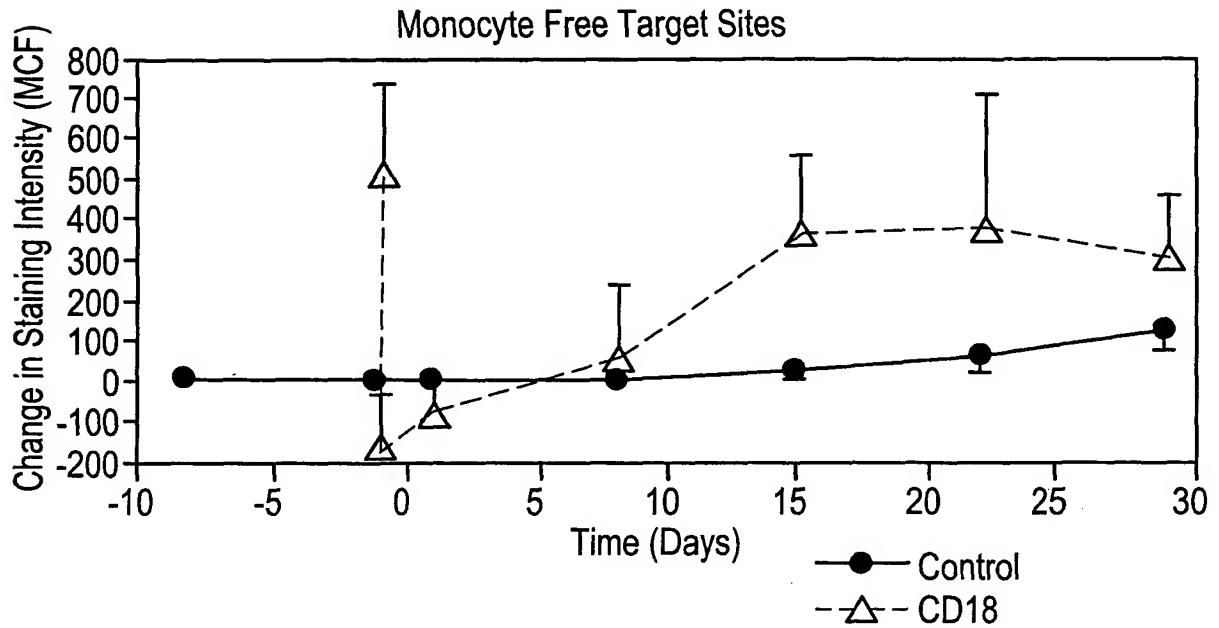


FIG. 3A

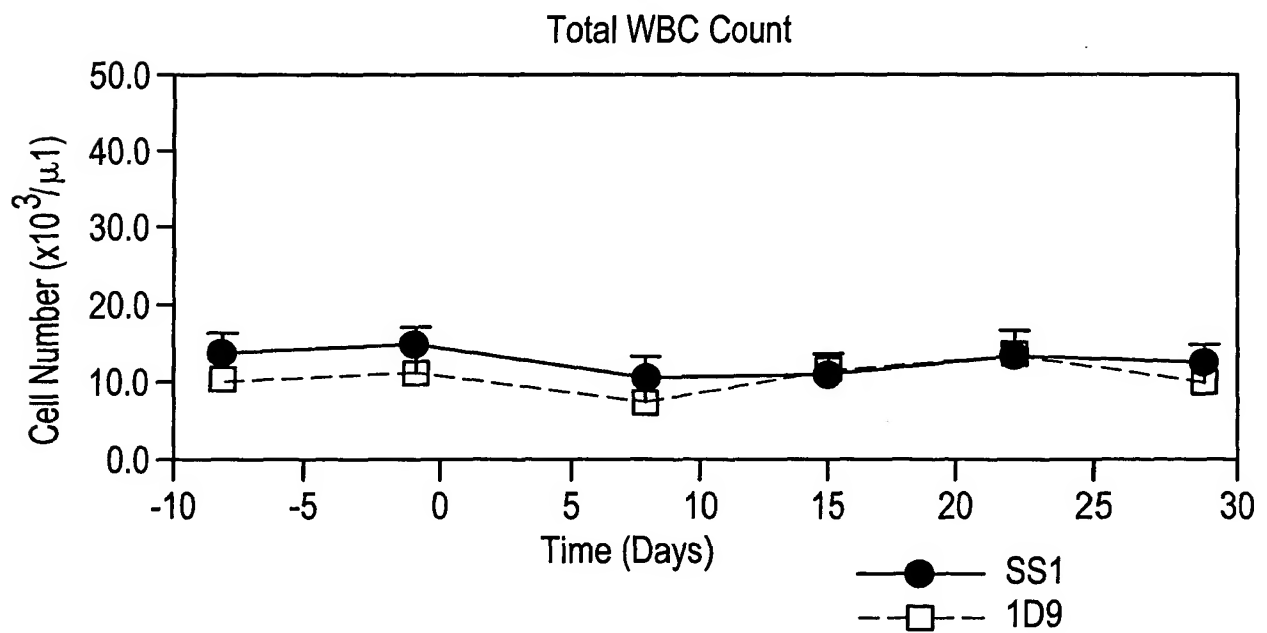


FIG. 3B

Total Neutrophil Count

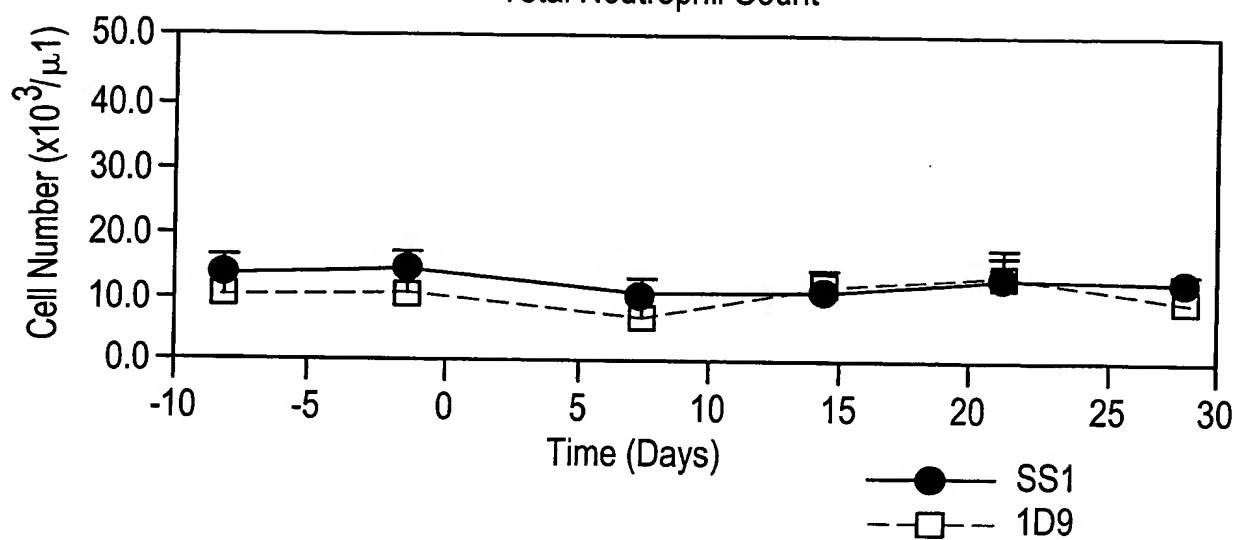


FIG. 3C

Total Lymphocyte Count

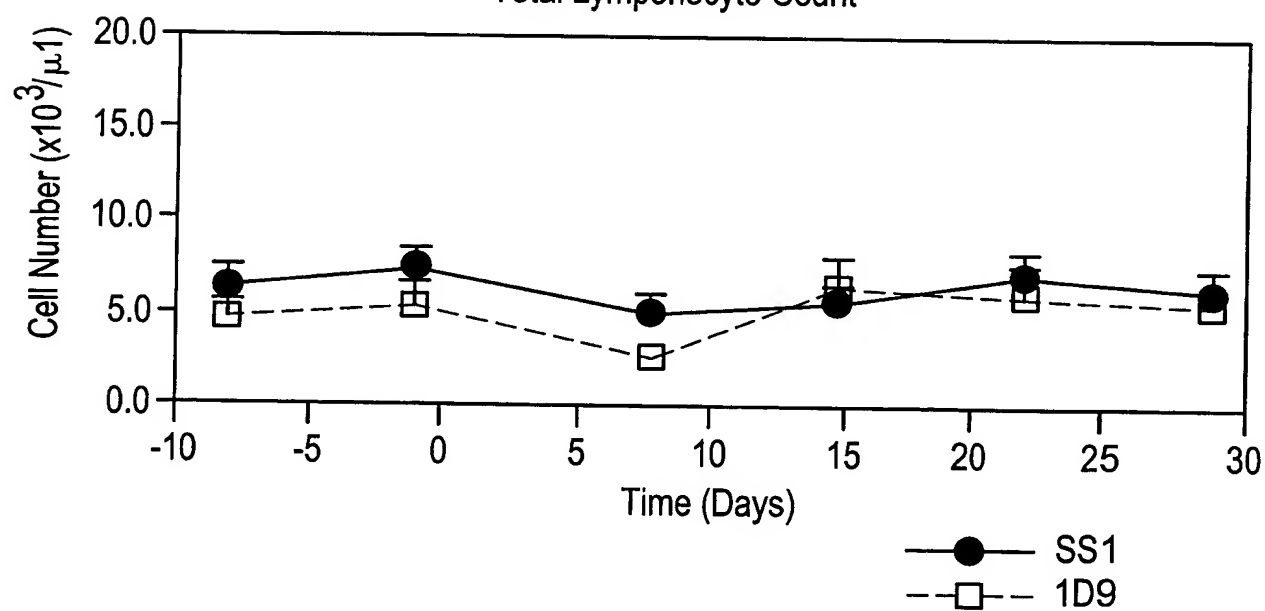


FIG. 3D

Total Monocyte Count

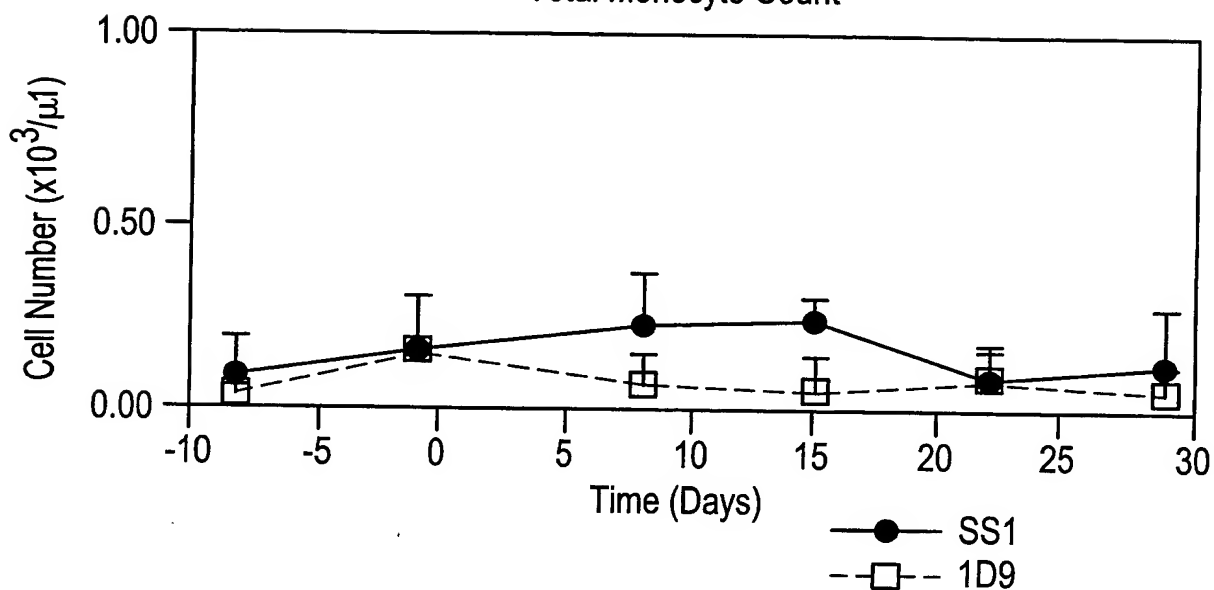


FIG. 3E

Total WBC Count

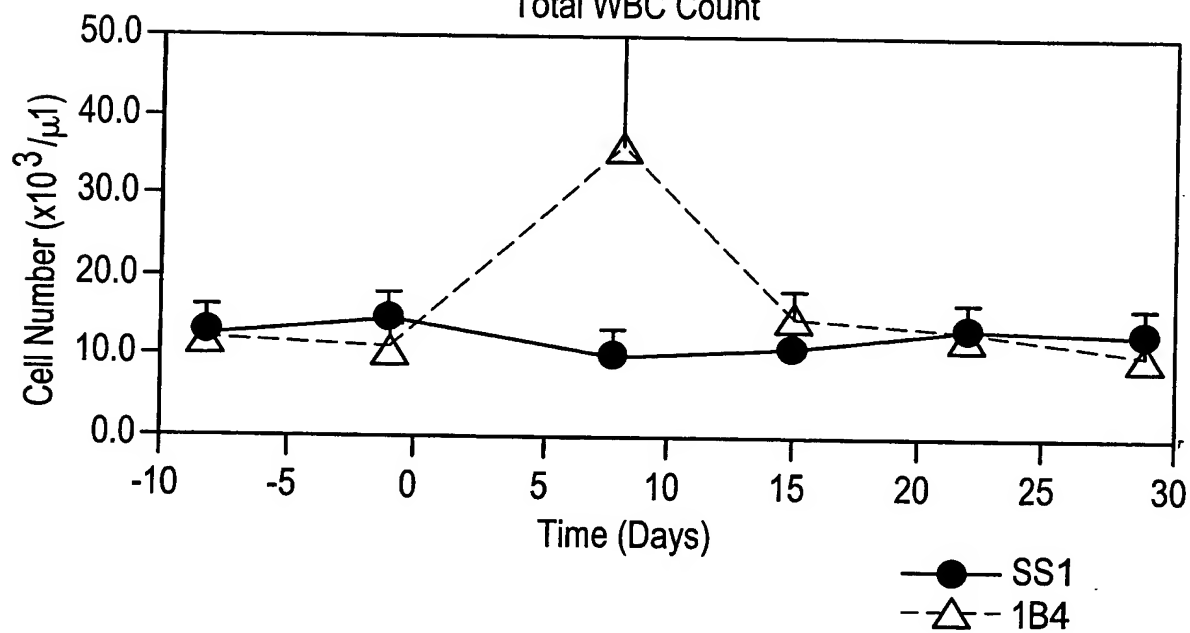


FIG. 3F

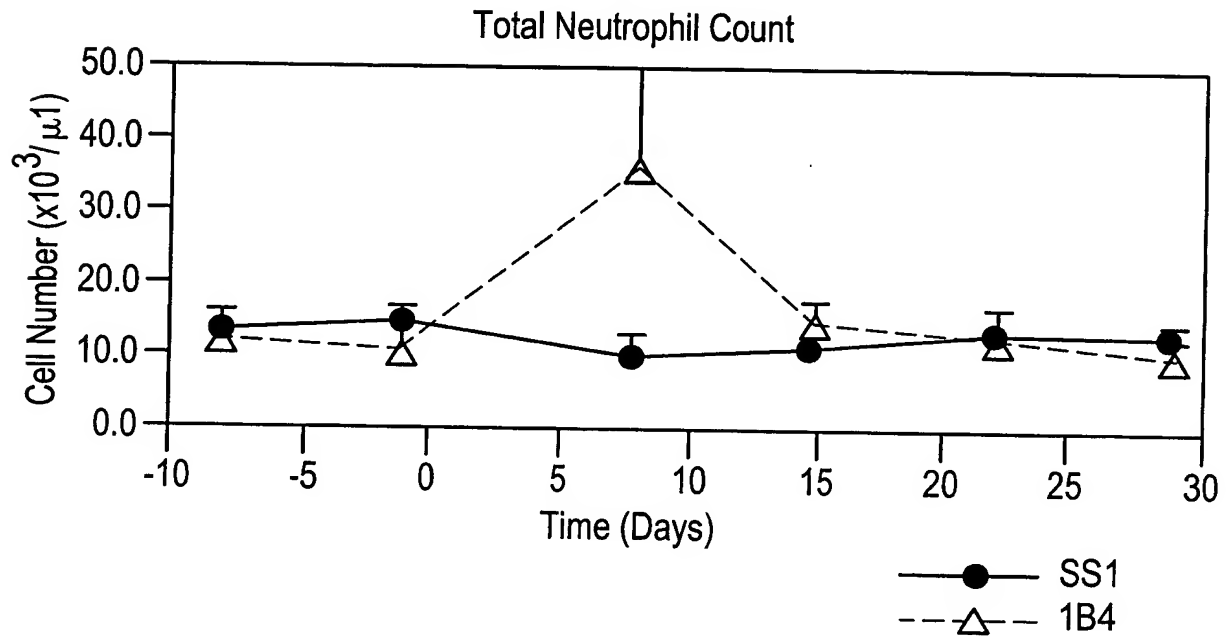


FIG. 3G

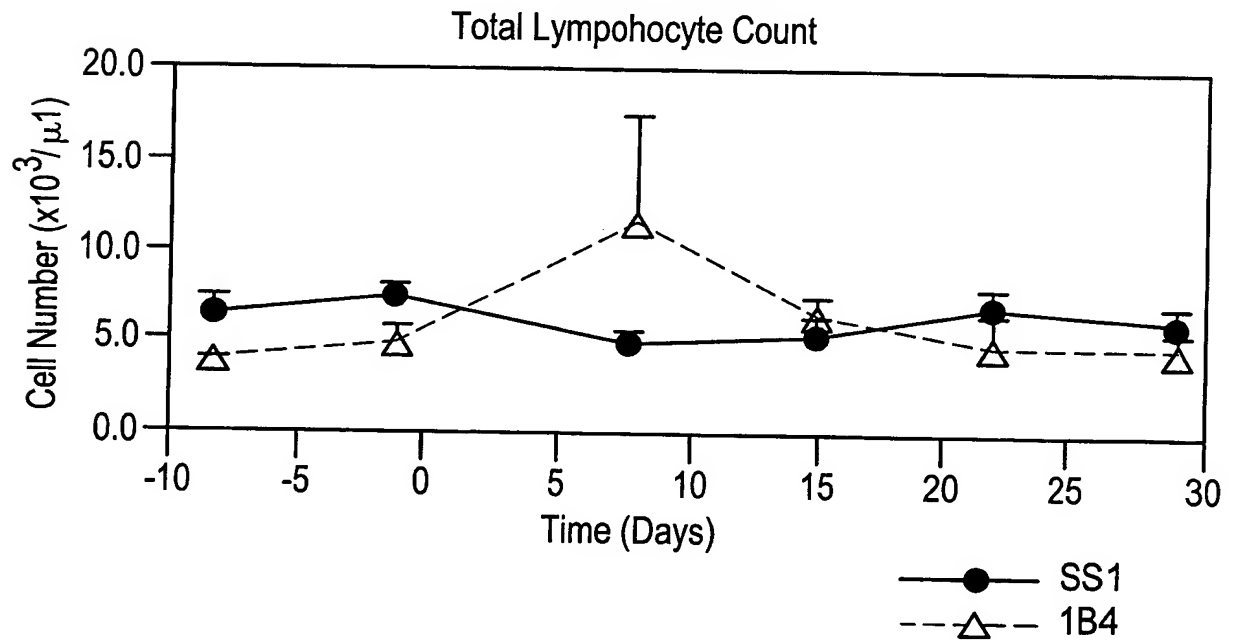


FIG. 3H

Total Monocyte Count

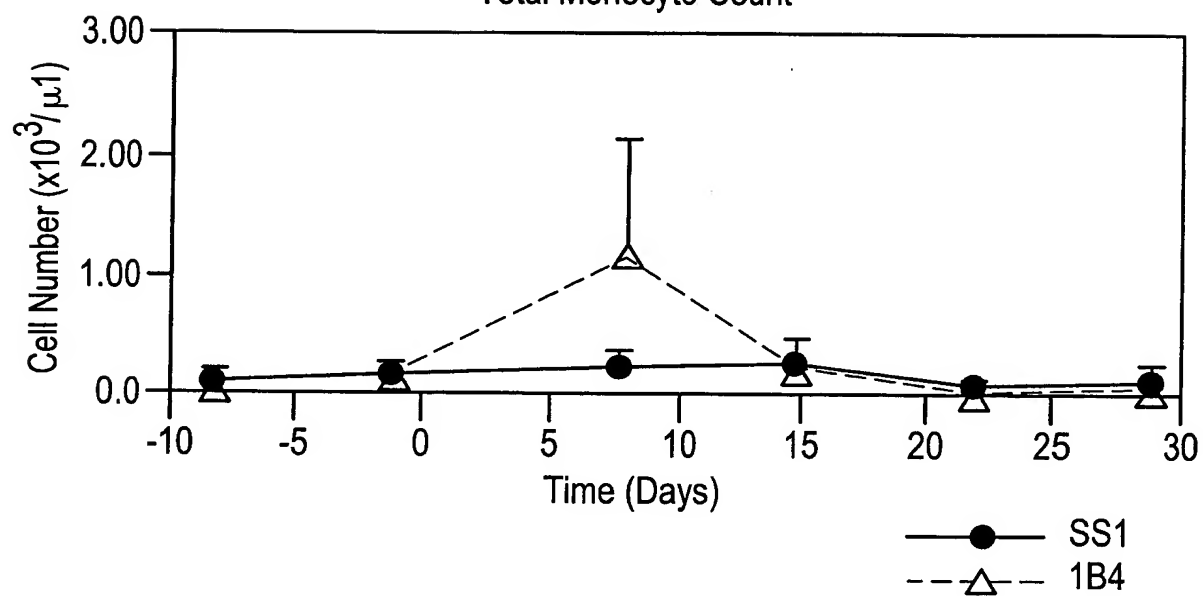


FIG. 4A

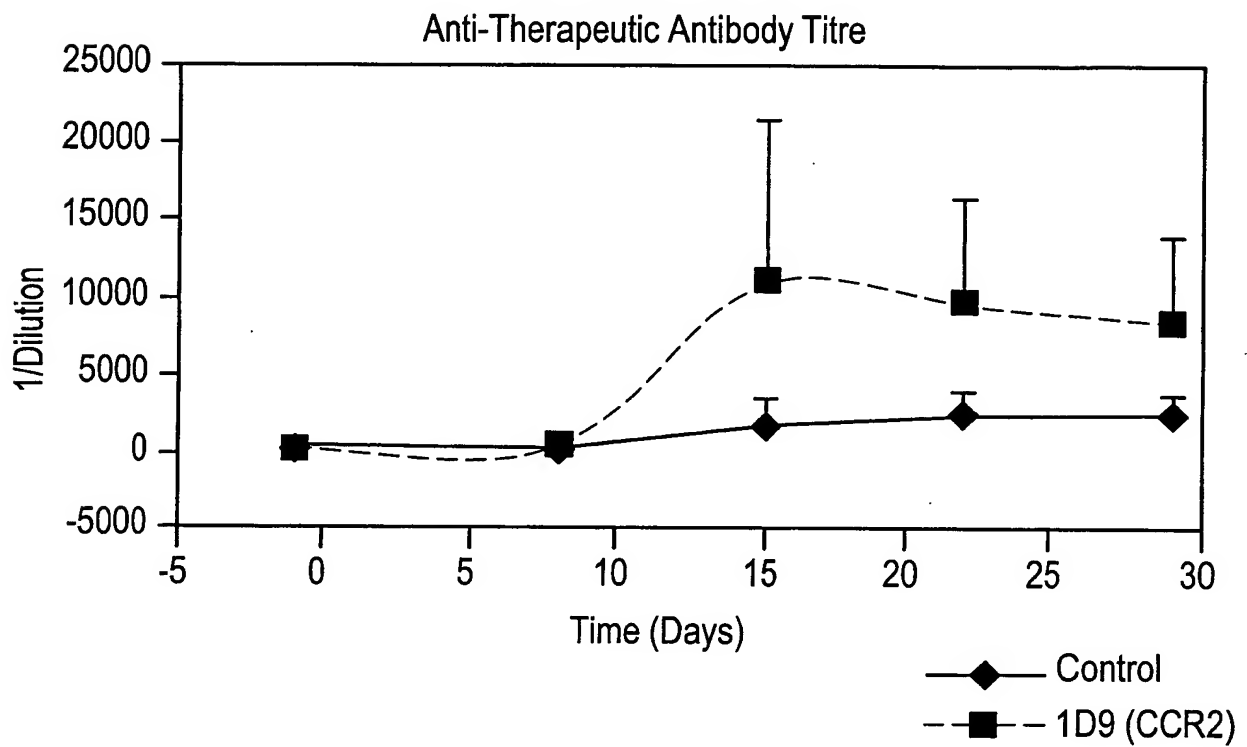


FIG. 4B

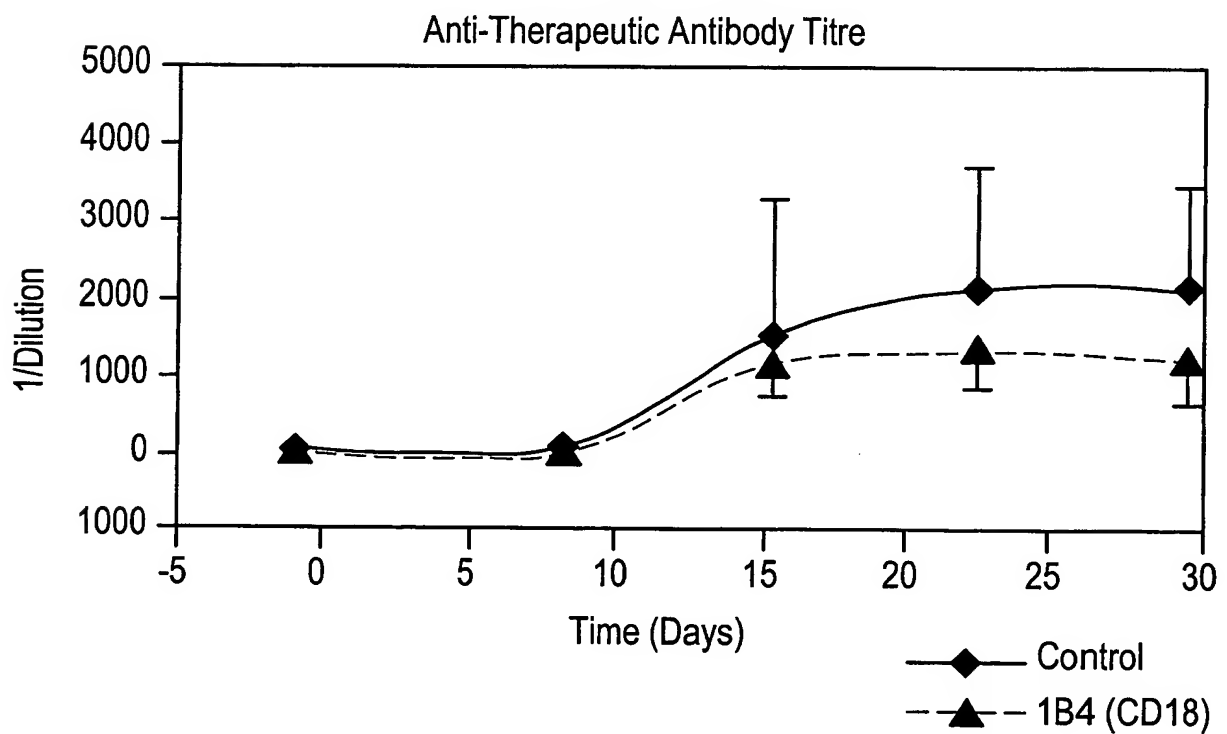


FIG. 5A

Luminal Diameter

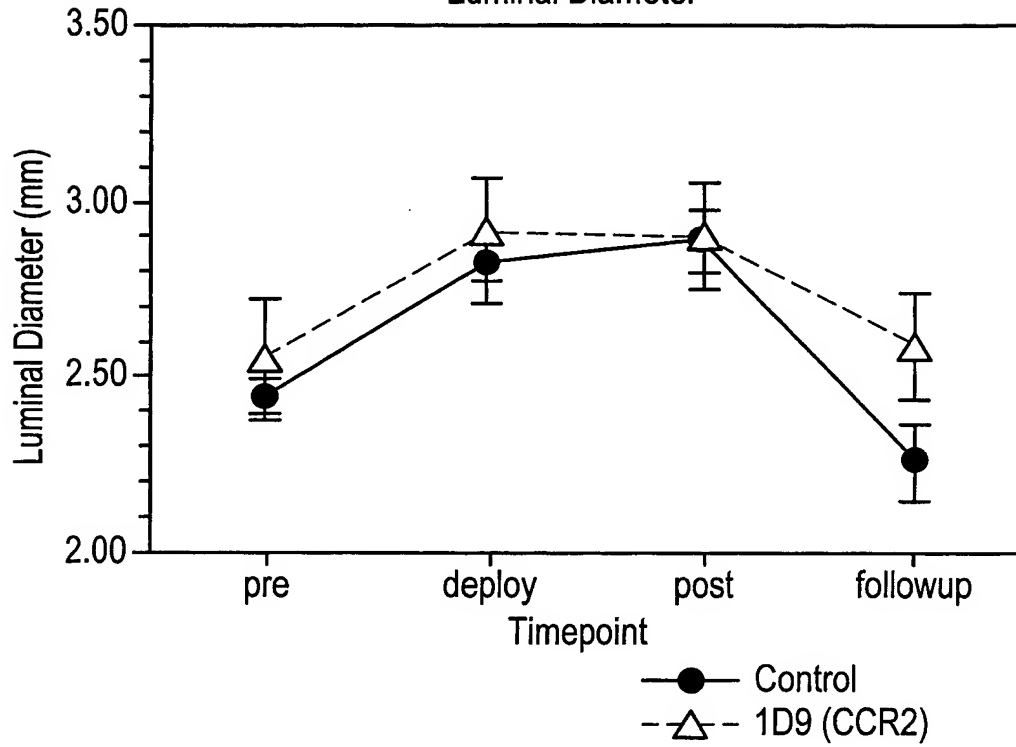


FIG. 5B

Late Luminal Loss

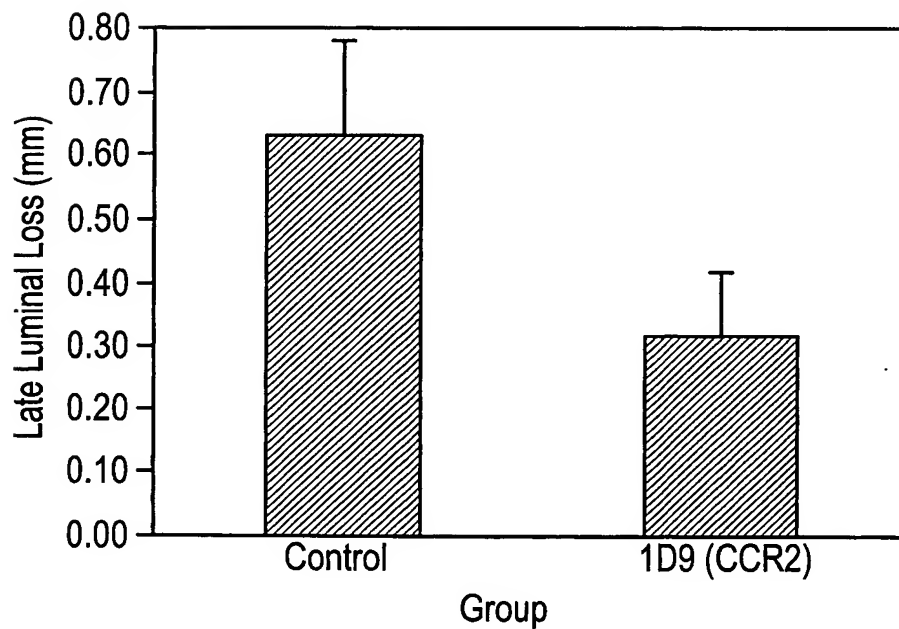


FIG. 5C

Index=LLL/ALG

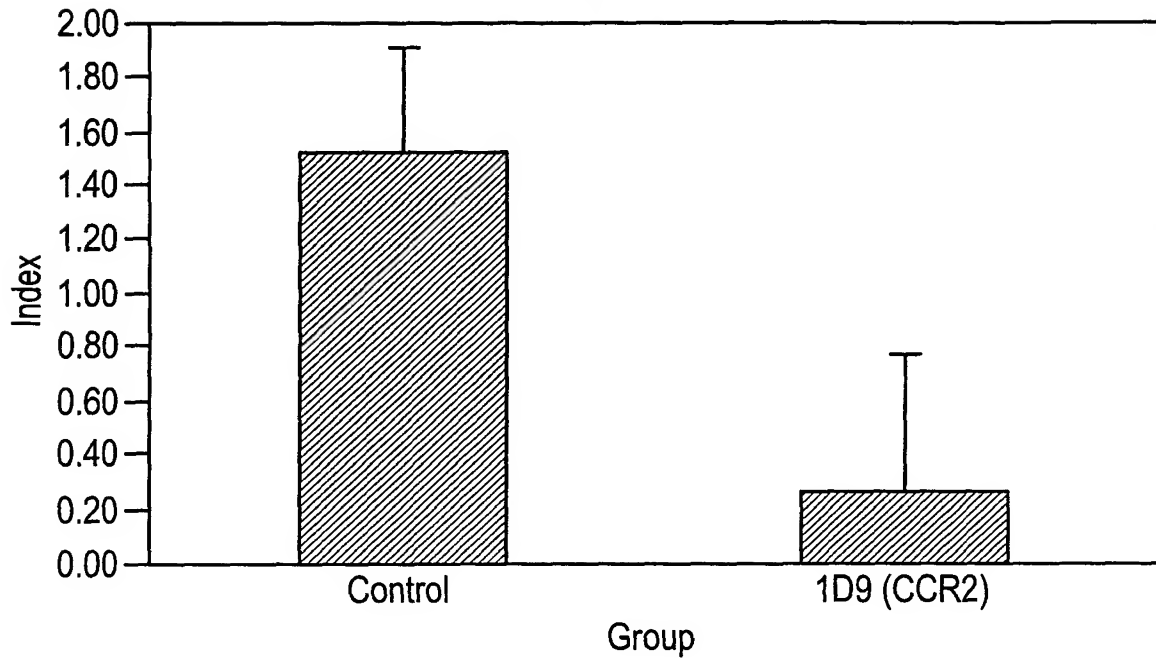


FIG. 5D

Luminal Diameter

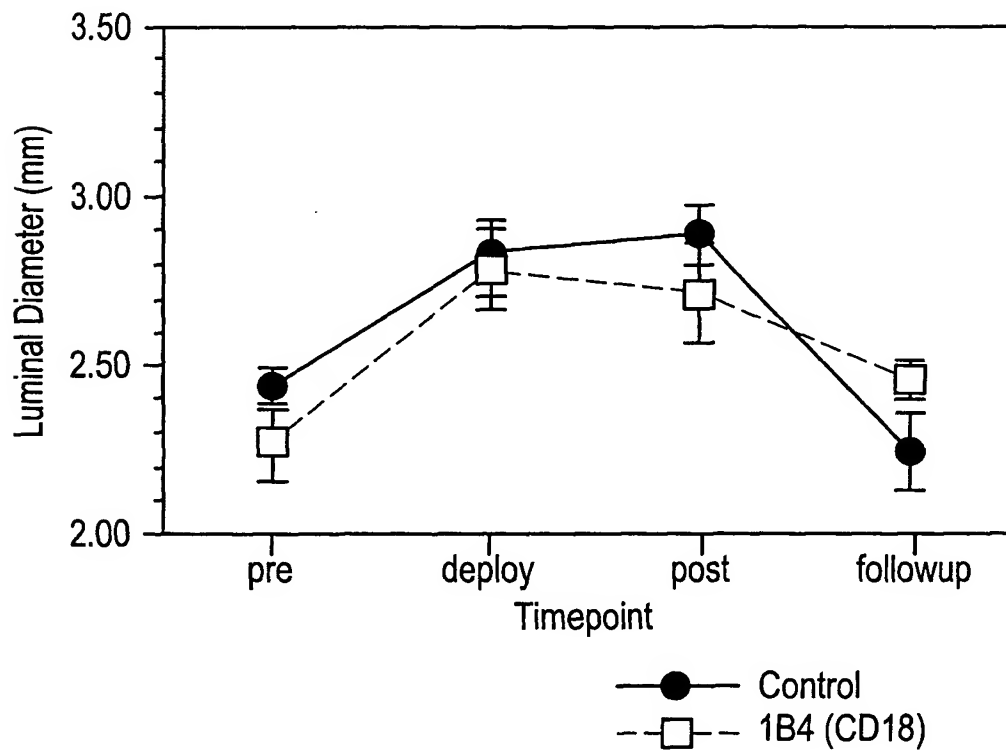


FIG. 5E

Late Luminal Loss

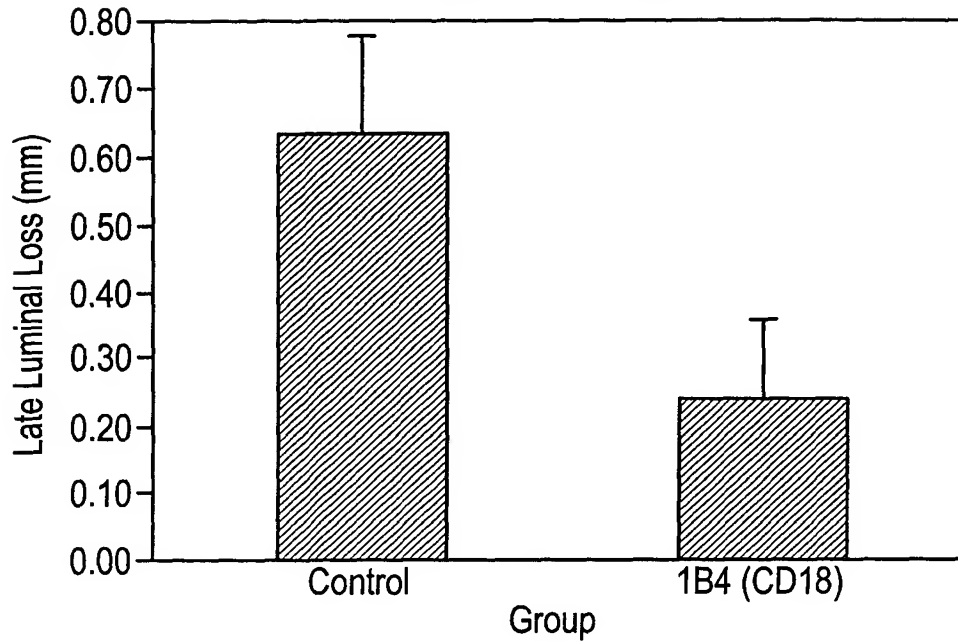


FIG. 5F

Index=LLL/ALG

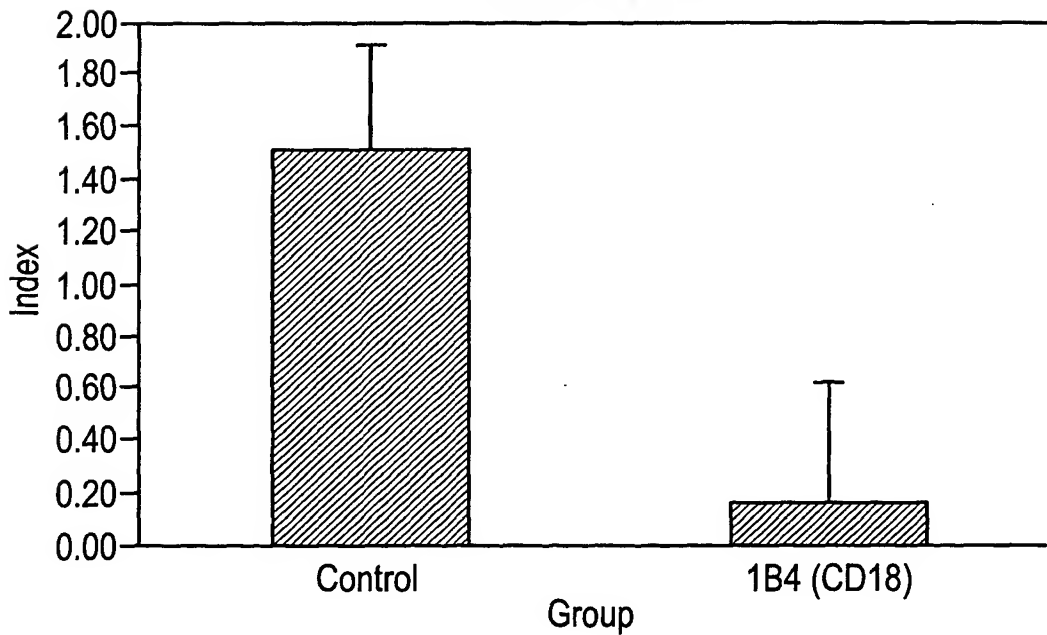


FIG. 6A

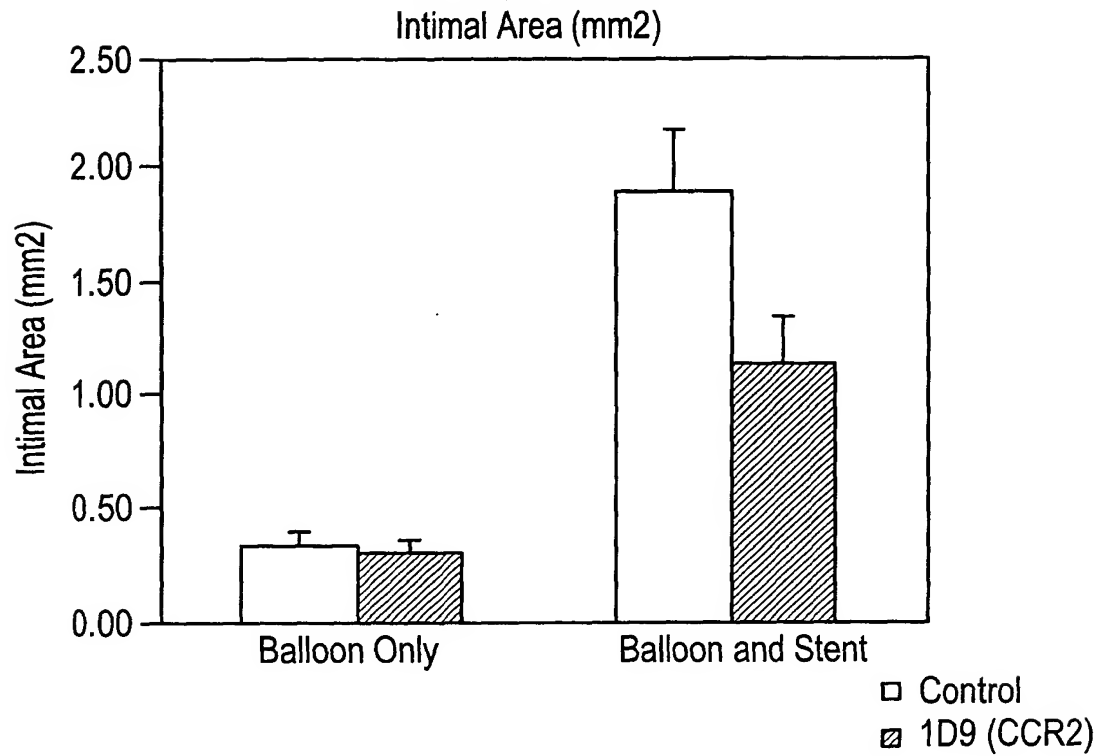


FIG. 6B

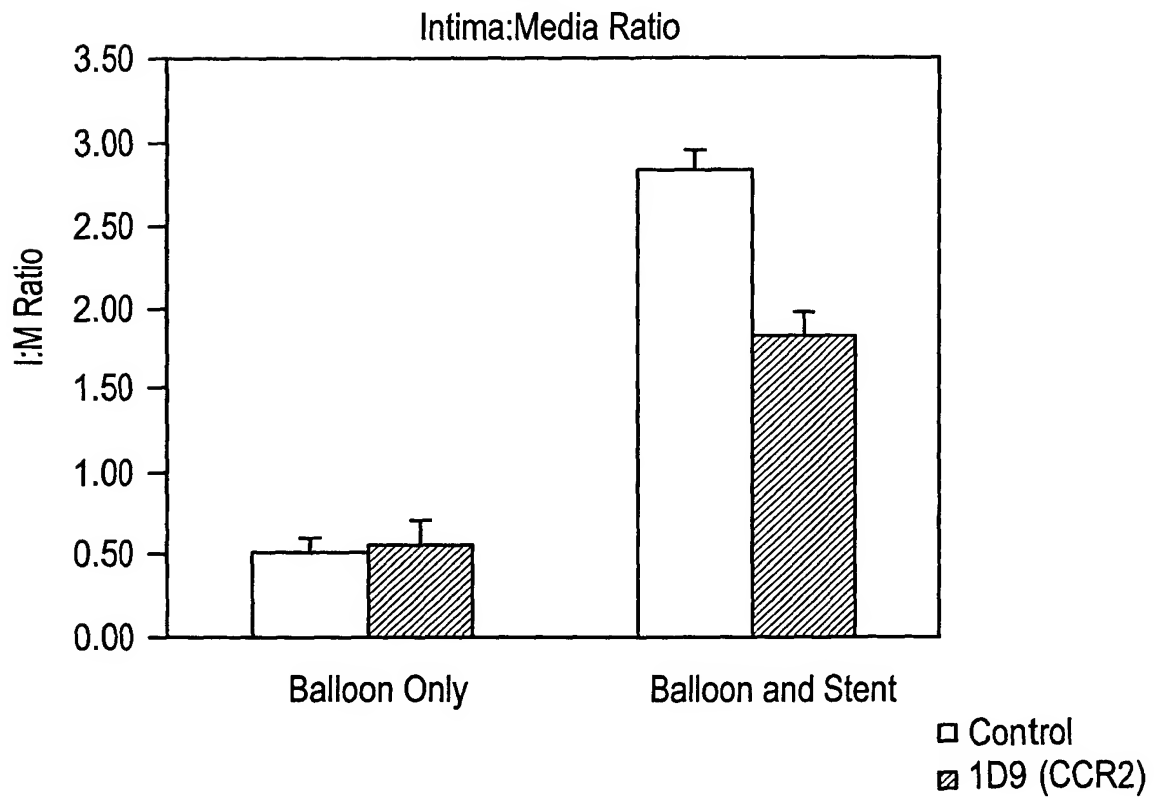


FIG. 6C

Intimal Area (mm²)

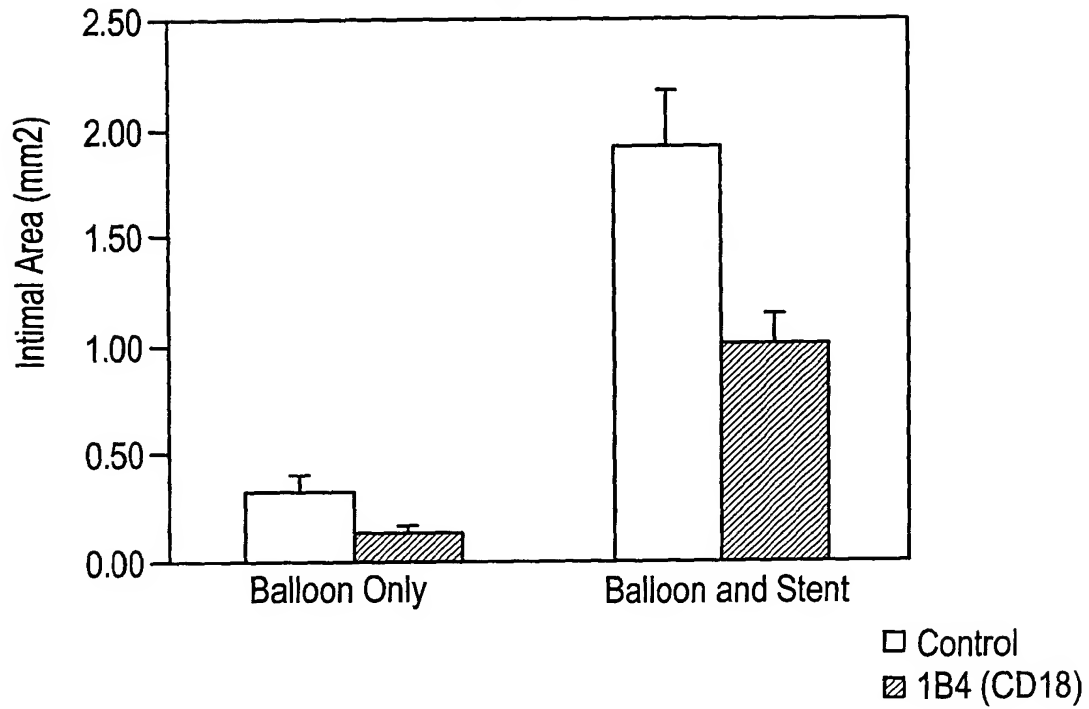
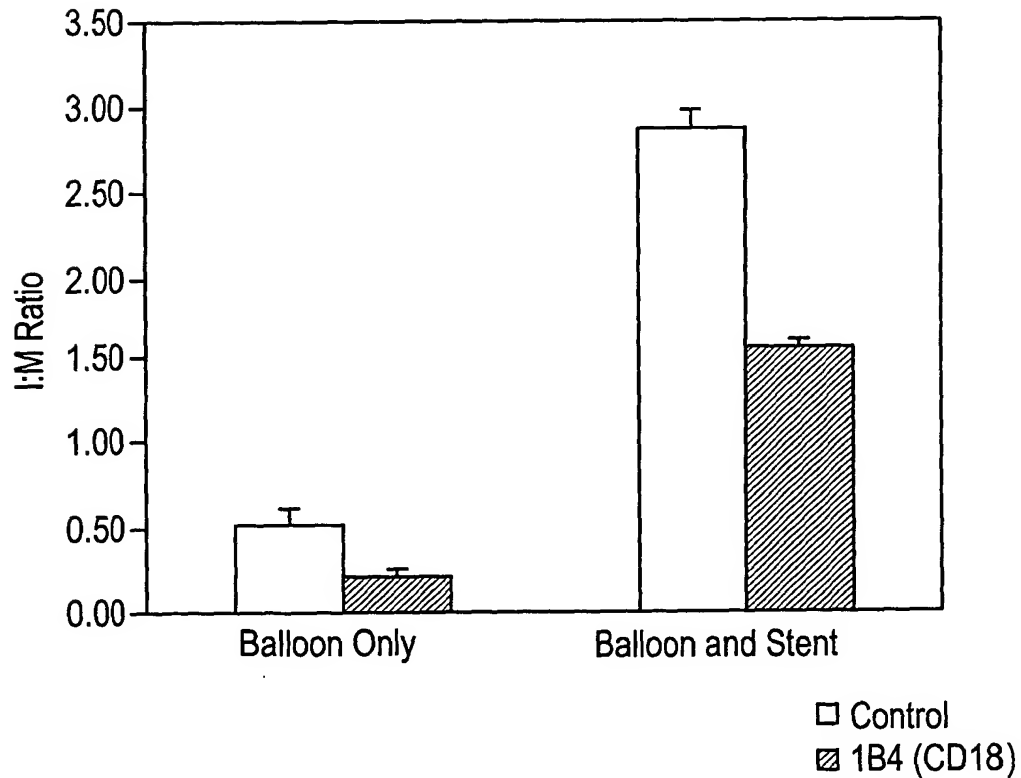


FIG. 6D

Intima:Media Ratio



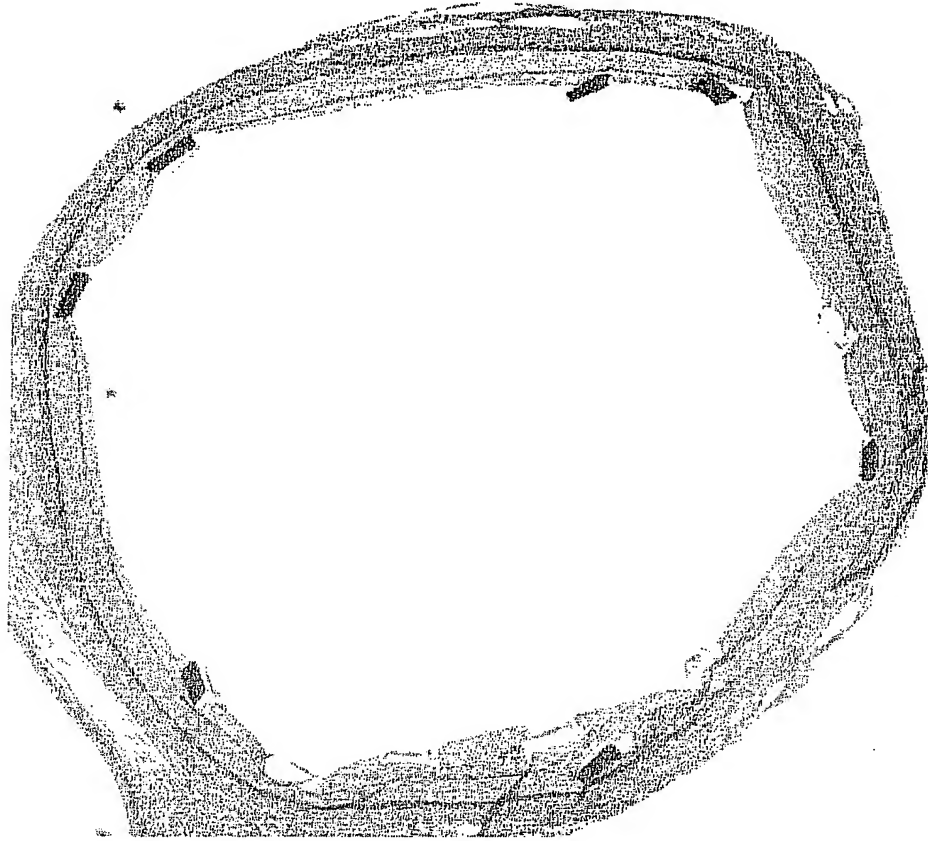


Fig. 7B

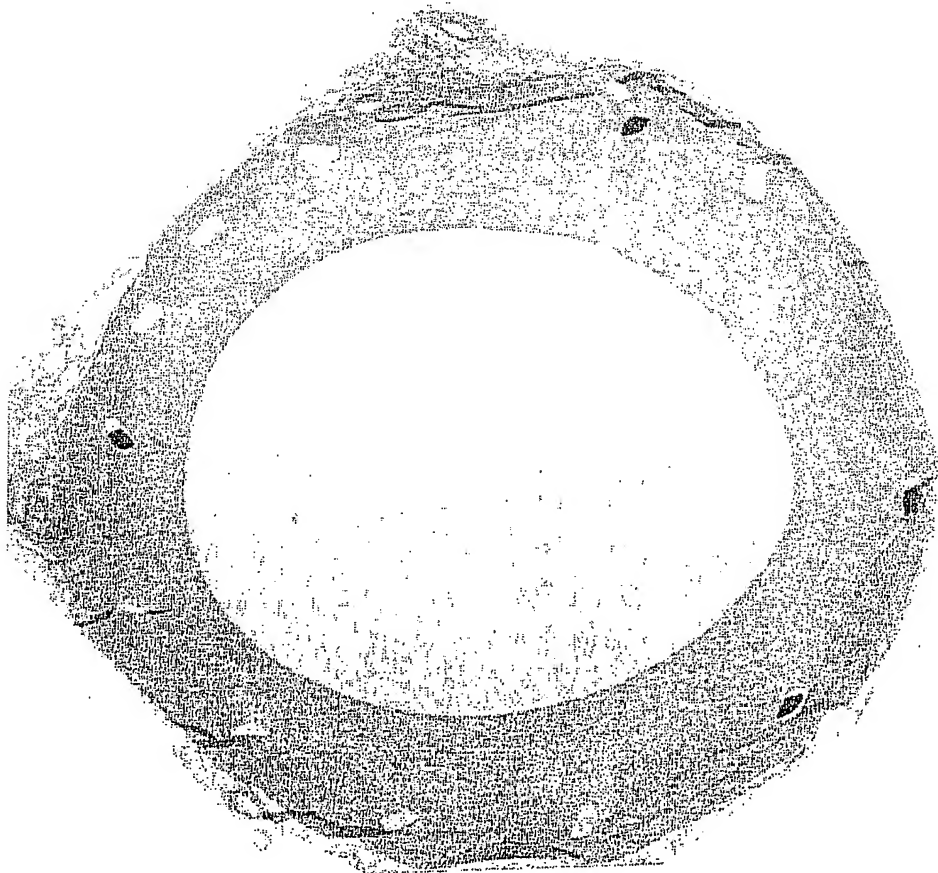


Fig. 7A

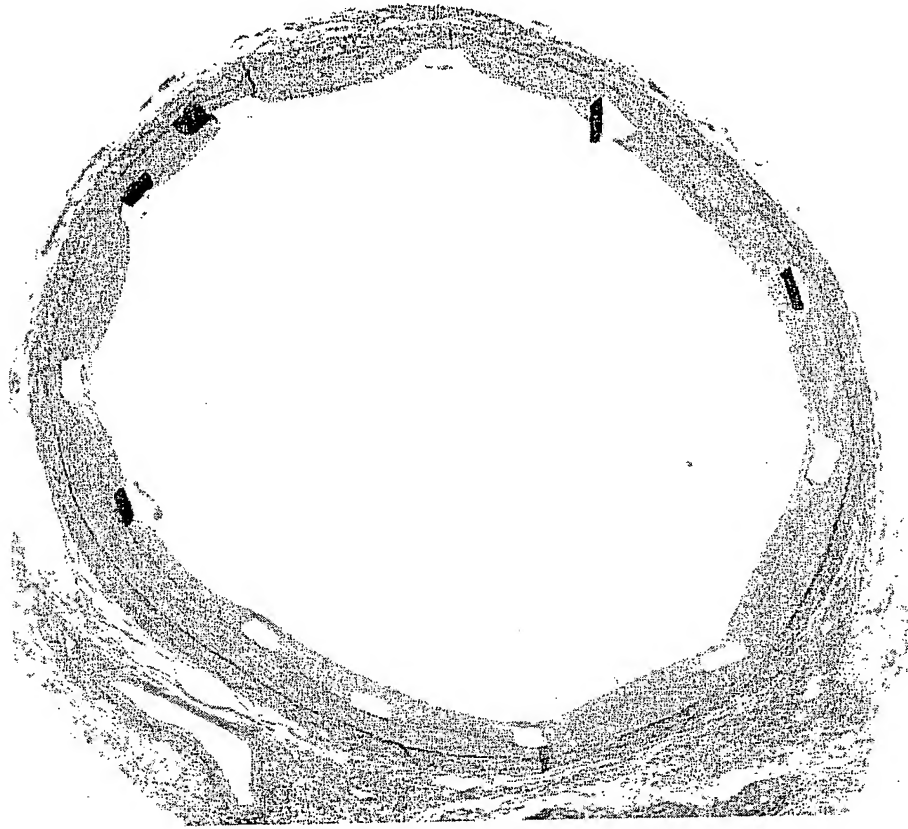


Fig. 8B

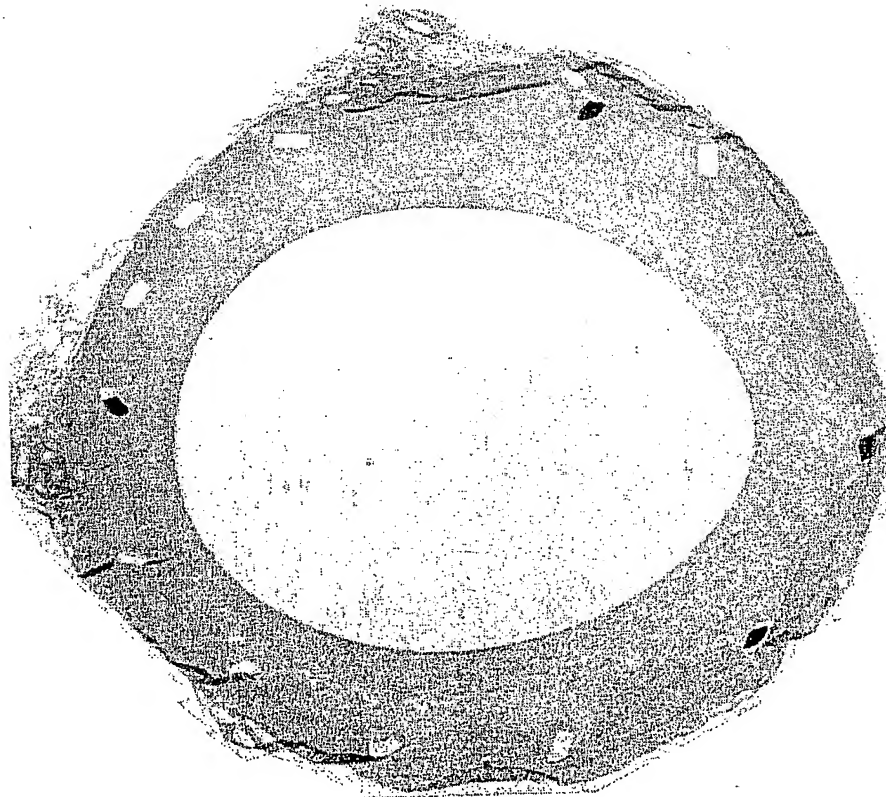


Fig. 8A

Met Arg Val Gln Val Gln Phe Leu Gly Leu Leu Leu Leu Thr Ser
Gly Ala Gln Cys Asp Val Gln Met Thr Gln Ser Pro Ser Tyr Leu Ala
Ala Ser Pro Gly Glu Ser Val Ser Ile Ser Cys Lys Ala Ser Lys Ser
Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Glu Ala Asn
Lys Leu Leu Val Tyr Tyr Gly Ser Thr Leu Arg Ser Gly Ile Pro Ser
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg
Asn Leu Glu Pro Ala Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
Glu Arg Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu

Fig. 9

CDR1	Lys Ala Ser Lys Ser Ile Ser Asn Tyr Leu Ala
CDR2	Tyr Gly Ser Thr Leu Arg Ser
CDR3	Gln Gln Tyr Tyr Glu Arg Pro Leu Thr

Fig. 10

Met Lys Cys Ser Trp Ile Asn Leu Phe Leu Met Ala Leu Ala Ser Gly

Val Tyr Ala Glu Val Gln Leu Gln Ser Gly Pro Glu Leu Arg Arg

Pro Gly Ser Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ser Ile

Lys Asp Tyr Leu Leu His Trp Val Lys His Arg Pro Glu Tyr Gly Leu

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Gly

Gln Lys Phe Gln Ser Arg Ala Thr Leu Thr Ala Asp Thr Ser Ser Asn

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Thr Ala Thr

Tyr Phe Cys Thr Arg Gly Glu Tyr Arg Tyr Asn Ser Trp Phe Asp Tyr

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

Fig. 11

CDR1	Asp Tyr Leu Leu His
CDR2	Trp Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Gly Gln Lys Phe Gln Ser
CDR3	Gly Glu Tyr Arg Tyr Asn Ser Trp Phe Asp Tyr

Fig. 12

1 MGWSCILFL VATATGVHSQ VQLQESGPGL VRPSQTLSLT CTVSGFTFTD
51 YLLHWVRQPP GRGLEWIGWIDPEDGETKYG QKFQSRVTML VDTSKNQFSL
101 RLSSVTAADT AVYYCARGEY RYNSWFDYWG QGSLVTVSS

Fig. 13

1 MGWSCILFL VATATGVHSD IQMTQSPSSL SASVGDRVTI TCKASKSISN
51 YLAWYQQKPG KAPKLLIYYG STLRSGVPSR FSGSGSGTDF TFTISSLQPE
101 DIATYYCQQY YERPLTFGQG TKVEIKR

Fig. 14

1 DVVMTQTPLT LSVTVGHPAS ISCKSSQSLL DSDGKTFLNW LLQRPGQSPK
51 RLIYLVSKLD SGVPDRFTGS GSGTDFTLKI SRVEAEDLGV YYCWQGTHFP
101 YTFGGGKLE IK

Fig. 15

1 EVQLVESGGG LVQPKGSLKL SCAASGFSFN AYAMNWVRQA PGKGLEWVAR
51 IRTKNNNYAT YYADSVKDRY TISRDDSESM LFLQMNNLKT EDTAMYYCVT
101 FYGNGVWGTG TTVTVSS

Fig. 16

[illegible]

CDRS	-----H1=====	=====H2=====	=====H3=====								
Kabat Numbers	1	2	3	4	5	6	7	8	9	1	1
	1234567890123456789012345678901234567890123456789012345678901234567890123										
1D9	EVQLVESGGGLVQPKGSLKLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIRTKNNNYATYYADSVKDRYTI	SRDDSESMFLQMN	NLKTEDTAMYYCVTFYGN-----	GVWGTGTTVT	VSS						
4B4'CL V _HK.G...R.....T.SNAW.SG..KS.TDGGT.D..AP..G.F.....	KNT.Y....S.....V...T.DSLPPH	R...Q..L.....							
1D9RH _A V _H	EVQLVESGGGLVQPKGSLRLSCAASGFTFSAYAMN--WVRQAPGKGLEWVGRI	RTKNNNYATYYADSVKDRFTI	SRDDSKNTLYLQMN	SLKTEDTAVYYCTTFYGN-----	GVWQGGTLVT	VSS					
1D9RH _B V _H	EVQLVESGGGLVQPKGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVGRI	RTKNNNYATYYADSVKDRFTI	SRDDSKNTLYLQMN	SLKTEDTAVYYCTTFYGN-----	GVWQGGTLVT	VSS					
1D9RH _C V _H	EVQLVESGGGLVQPKGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIR	TKNNNYATYYADSVKDRYTI	SRDDSKNTLYLQMN	SLKTEDTAVYYCTTFYGN-----	GVWQGGTLVT	VSS					
1D9RH _D V _H	EVQLVESGGGLVQPKGSLRLSCAASGFSFNAYAMN--WVRQAPGKGLEWVARIR	TKNNNYATYYADSVKDRYTI	SRDDSKNTLYLQMN	SLKTEDTAVYYCTTFYGN-----	GVWQGGTLVT	VSS					
Key											
1D9 V _H	Mouse 1D9 V _H region.										
4B4'CL V _H	Chosen human framework acceptor V _H region sequence with mismatches to the 1D9 V _H region highlighted.										
1D9RH _A V _H	CDR grafted 1D9 V _H region, with no back mutations.										
1D9RH _B V _H	CDR grafted 1D9 V _H region, with back mutations at T28S and S30N.										
1D9RH _C V _H	CDR grafted 1D9 V _H region, with back mutations at T28S, S30N, G49A and F67Y.										
1D9RH _D V _H	CDR grafted 1D9 V _H region, with back mutations at T28S, S30N, G49A, F67Y and T93V.										

Fig. 18